

## SEQUENCE LISTING

<110> Ullman, Katharine  
Liu, Jin  
Prunuske, Amy  
Dimaano, Christian

<120> METHODS AND COMPOSITIONS RELATED TO  
INHIBITING NUCLEAR ENVELOPE BREAKDOWN

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<151> 2003-09-17

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<223> Description of Artificial Sequence:/note =  
synthetic construct

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Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
 65           70           75           80
Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
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Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
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&lt;211&gt; 1200

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

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gcaaaaccag	cagcacactc	tcagcagtg	ggtgttacca	gctccgctgc	acgccgcatt	960
ctacagtctt	tggagaagat	gtcaagtcct	ttagcggatg	ccaaaaggat	cccatcaaac	1020
tcttctttat	cacatacacc	agaaaagaac	gtcatggata	ttcccgaaaa	cccatcaaaa	1080
aggaaaaagg	tggagtcccc	atttcctcca	gttcagaggc	tcgtgactcc	aaaatccatt	1140
tctgtctctg	caaaccgttc	cctgtatatc	aagccttcac	tgacaccatc	tgctgtatca	1200

&lt;210&gt; 4

&lt;211&gt; 400

&lt;212&gt; PRT

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 4

Met	Ala	Ala	Ala	Gly	Gly	Gly	Gly	Pro	Gly	Gly	Pro	Gly	Thr	Gly	Gly
1				5					10					15	
Lys	Ile	Arg	Ser	Arg	Arg	Tyr	His	Leu	Ser	Ser	Gly	Arg	Thr	Pro	Tyr
			20					25				30			
Ser	Lys	Ser	Arg	Gln	Arg	Gln	Gln	Gly	Ile	Ile	Ser	Arg	Val	Thr	Asp
		35				40					45				
Thr	Val	Lys	Ser	Ile	Val	Pro	Gly	Trp	Leu	Gln	Lys	Tyr	Phe	Asn	Lys
	50					55					60				
Gln	Glu	Glu	Glu	His	Asp	Arg	Val	His	Ser	Ala	Ser	Glu	Val	Ile	Val
65				70						75				80	
Asn	Asp	Thr	Glu	Ala	Arg	Glu	Asn	Asn	Ala	Gln	His	His	Ile	Tyr	Asp
			85					90						95	
Asp	Asp	Asp	Glu	Glu	Gly	Asn	Ser	Pro	Thr	Asp	Gly	Arg	Val	Thr	Pro
		100				105						110			
Glu	Pro	Val	Ile	Asn	Val	Asp	Glu	Glu	Val	Pro	Ser	Thr	Ser	Gln	Ser
		115				120						125			
Ala	Ile	Asn	Asn	Thr	Asp	Ala	Leu	Thr	Arg	Pro	Ser	Leu	His	Arg	Ala
	130					135				140					
Ser	Leu	Asn	Phe	Asn	Ile	Phe	Asp	Ser	Pro	Ala	Leu	Asn	Cys	Gln	Pro
145				150						155				160	
Ser	Thr	Ser	Ser	Ala	Phe	Pro	Ile	Gly	Thr	Ser	Gly	Phe	Ser	Leu	Ile
			165					170						175	
Lys	Glu	Ile	Lys	Asp	Ser	Thr	Ser	Gln	His	Asp	Asp	Asp	Asn	Ile	Ser
			180					185					190		
Thr	Thr	Ser	Gly	Phe	Thr	Ser	Arg	Ala	Ser	Asp	Lys	Asp	Leu	Ala	Val
	195					200					205				
Ser	Lys	Asn	Val	Ser	Val	Pro	Pro	Leu	Trp	Ser	Pro	Glu	Val	Asp	Arg
	210					215				220					
Ser	Gln	Ser	Leu	Ser	His	Asn	Ser	Ser	Met	Thr	Ser	Lys	Lys	Pro	Thr
225				230					235					240	
Phe	Asn	Leu	Ser	Ala	Phe	Gly	Ser	Leu	Ser	Pro	Ser	Leu	Gly	Asn	Ala
			245					250						255	
Ser	Ile	Leu	Asn	Arg	Gln	Leu	Gly	Asp	Ser	Pro	Phe	Tyr	Pro	Gly	Lys
		260						265					270		
Thr	Thr	Tyr	Gln	Gly	Ala	Ala	Ala	Val	Arg	Ser	Ser	Arg	Val	Arg	Ala
	275					280						285			
Thr	Pro	Tyr	Gln	Ala	Pro	Leu	Arg	Arg	Gln	Val	Lys	Ala	Lys	Pro	Ala
	290					295				300					
Ala	His	Ser	Gln	Gln	Cys	Gly	Val	Thr	Ser	Ser	Ala	Ala	Arg	Arg	Ile
305				310						315				320	
Leu	Gln	Ser	Leu	Glu	Lys	Met	Ser	Ser	Pro	Leu	Ala	Asp	Ala	Lys	Arg
			325					330						335	
Ile	Pro	Ser	Asn	Ser	Ser	Leu	Ser	His	Thr	Pro	Glu	Lys	Asn	Val	Met
		340						345					350		
Asp	Ile	Pro	Glu	Asn	Pro	Ser	L								

<210> 5

<211> 4305

<212> DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 5

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atctcagctc	cacagcttct	cttaccctaaa	gttcagtact	ccggcatcca	atggattgtc	180
atcaggaaca	ggtggtggca	aaatgatgag	ggaaaaaggc	tctcattact	caacaaagcc	240
agctaattag	gagctggatg	ggcctgtttt	acctgaaatc	ccattgcctc	ttagcacagc	300
agcccttccc	agctttcaat	tttcaacttt	gtctggctct	gctacttcgc	ctatctctgt	360
cactaaacct	gcaaacagta	cgacatgtca	cttaaccagc	agtagtccat	cgttcacatt	420
ttcgtccctt	attgtaaaat	cgactgaatc	aaatgctcag	ttttctggct	catctgttga	480
tttcactttc	agtgtaccag	cagcgaaagc	gtcatctgca	acatctgatg	agagcaaggt	540
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tgatgatgaa	caagtgggat	tctgtaaaacc	tgcaaaaact	ctgaaggaag	ggagtgtgtt	660
agacatgctg	agaagtccag	ggttttcttc	tttaccctcc	ctgctaactt	cagaatcaac	720
tcttaacaga	agcacacaa	cctctcaaa	gactgtgggg	aatacattct	cccctgcaaa	780
tgatcatta	ggaagtggaa	gcaagcaatt	tggactttgg	caatgcagcg	catgctttca	840
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caaacctggg	acttgtataa	aagctacctt	gttgataccg	tccaccacaa	agtctataaa	1140
tccagccaca	aatacccttg	cttttgcctc	ttgctctgca	agcattccaa	atgaagaaat	1200
gttcaaaaag	cctatgggat	cttgggagtg	cacagtttgt	catatgcaga	ataaaacaga	1260
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aagttttaac	tttggacgaa	caatcacttc	aaatacaaca	ggcactagct	cgtctccatt	3180
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tcattcagct cttgtcatct tctccattat tttattatat tcatgtaa atacattgttt 4260
ctccatgtac ctttcagcat aaactaaatc aaaaaaaaaa aaaaaa 4305

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&lt;210&gt; 6

&lt;211&gt; 1219

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 6

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Ala Asn Arg Ser Leu Tyr Ile Lys Pro Ser Leu Thr Pro Ser Ala Val
 1              5              10              15
Ser Asn Thr Asn Ser Arg Arg Ile Gln Pro Asp Lys His Asn Glu Ser
 20              25              30
Thr Lys Asn Asn Leu Gln Ser Thr Ser Gln Ser His Ser Phe Ser Tyr
 35              40              45
Pro Lys Phe Ser Thr Pro Ala Ser Asn Gly Leu Ser Ser Gly Thr Gly
 50              55              60
Gly Gly Lys Met Met Arg Glu Lys Gly Ser His Tyr Ser Thr Lys Pro
 65              70              75              80
Ala Asn Glu Glu Leu Asp Gly Pro Val Leu Pro Glu Ile Pro Leu Pro
 85              90              95
Leu Ser Thr Ala Ala Leu Pro Ser Phe Gln Phe Ser Thr Leu Ser Gly
 100             105             110
Ser Ala Thr Ser Pro Ile Ser Val Thr Lys Pro Ala Asn Ser Thr Thr
 115             120             125
Cys His Leu Thr Ser Ser Ser Pro Ser Phe Thr Phe Ser Ser Pro Ile
 130             135             140
Val Lys Ser Thr Glu Ser Asn Ala Gln Phe Ser Gly Ser Ser Val Asp
 145             150             155             160
Phe Thr Phe Ser Val Pro Ala Ala Lys Ala Ser Ser Ala Thr Ser Asp
 165             170             175
Glu Ser Lys Val Ser Ala Val Ser Ser Ala Ala Lys Thr His Ala Ala
 180             185             190
Val Asn Ser Ser Ala Lys Asn Thr Asp Asp Glu Gln Val Gly Phe Cys
 195             200             205
Lys Pro Ala Lys Thr Leu Lys Glu Gly Ser Val Leu Asp Met Leu Arg
 210             215             220
Ser Pro Gly Phe Ser Ser Leu Pro Ser Leu Leu Thr Ser Glu Ser Thr
 225             230             235             240
Leu Asn Arg Ser Thr Pro Thr Leu Ser Lys Thr Val Gly Asn Thr Phe
 245             250             255

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Ser	Pro	Ala	Asn	Val	Ser	Leu	Gly	Val	Gly	Ser	Lys	Gln	Phe	Gly	Leu		
			260					265					270				
Trp	Gln	Cys	Ser	Ala	Cys	Phe	His	Glu	Asn	Met	Ser	Ser	Asp	Ser	Asn		
		275					280					285					
Cys	Ile	Ser	Cys	Ser	Ala	Val	Lys	Pro	Arg	Pro	Thr	Glu	Thr	Ser	Lys		
	290					295					300						
Lys	Leu	Pro	Ala	Ser	Pro	Pro	Ser	Ser	Asn	Thr	Lys	Ser	Thr	Val	Pro		
305					310					315					320		
Leu	Ser	Ser	Thr	Pro	Gly	Leu	Gly	Asp	Ile	Phe	Lys	Lys	Pro	Ala	Gly		
				325					330					335			
Met	Trp	Asp	Cys	Asp	Thr	Cys	Leu	Val	Gln	Asn	Lys	Ala	Glu	Val	Thr		
			340					345					350				
Lys	Cys	Val	Ala	Cys	Glu	Thr	Pro	Lys	Pro	Gly	Thr	Cys	Ile	Lys	Ala		
		355					360					365					
Thr	Leu	Leu	Ile	Pro	Ser	Thr	Thr	Lys	Ser	Ile	Asn	Pro	Ala	Thr	Asn		
	370					375					380						
Thr	Leu	Ala	Phe	Ala	Ser	Cys	Ser	Ala	Ser	Ile	Pro	Asn	Glu	Glu	Met		
385					390					395					400		
Phe	Lys	Lys	Pro	Met	Gly	Ser	Trp	Glu	Cys	Thr	Val	Cys	His	Met	Gln		
				405					410					415			
Asn	Lys	Thr	Glu	Asp	Asn	Thr	Cys	Val	Gly	Cys	Lys	Ala	Glu	Lys	Pro		
			420					425					430				
Gly	Thr	Val	Lys	Ser	Val	Pro	Thr	Ala	Ala	Pro	Ser	Gly	Leu	Leu	Gly		
		435					440					445					
Leu	Leu	His	Gln	Phe	Lys	Lys	Pro	Thr	Gly	Ser	Trp	Asp	Cys	Asp	Val		
	450					455					460						
Cys	Leu	Ile	Gln	Asn	Lys	Pro	Glu	Ala	Ala	Lys	Cys	Ile	Ala	Cys	Glu		
465					470					475					480		
Ser	Ala	Lys	Pro	Gly	Thr	Lys	Ala	Glu	Pro	Lys	Gly	Thr	Phe	Asp	Thr		
				485					490					495			
Val	Lys	Asn	Ser	Val	Ser	Val	Ala	Pro	Leu	Ser	Ser	Gly	Gln	Leu	Gly		
			500					505					510				
Leu	Leu	Asp	Gln	Phe	Lys	Lys	Ser	Ala	Gly	Ser	Trp	Asp	Cys	Asp	Val		
		515					520					525					
Cys	Leu	Val	Glu	Asn	Lys	Pro	Glu	Ala	Thr	Lys	Cys	Val	Ala	Cys	Glu		
	530					535					540						
Thr	Ser	Lys	Pro	Gly	Thr	Lys	Ala	Glu	Leu	Lys	Gly	Phe	Gly	Thr	Ser		
545					550					555					560		
Thr	Phe	Ser	Ser	Gly	Thr	Ala	Ala	Pro	Thr	Phe	Lys	Phe	Gly	Val	Gln		
				565					570					575			
Ser	Ser	Asp	Ser	Thr	Ala	Glu	Leu	Lys	Ser	Gly	Ala	Ser	Thr	Ser	Gly		
			580					585					590				
Phe	Ala	Lys	Ser	Ile	Gly	Asp	Phe	Lys	Phe	Gly	Leu	Val	Ser	Ala	Ser		
		595					600					605					
Thr	Thr	Thr	Glu	Glu	Thr	Gly	Lys	Lys	Ser	Phe	Thr	Phe	Gly	Ser	Ser		
	610					615					620						
Thr	Thr	Asn	Glu	Val	Ser	Ala	Gly	Phe	Lys	Phe	Gly	Ile	Ala	Gly	Ser		
625					630					635					640		
Ala	Gln	Thr	Lys	Pro	Asp	Thr	Leu	Ser	Gln	Ser	Thr	Thr	Ser	Gly	Phe		
				645					650					655			
Thr	Phe	Gly	Ser	Val	Ser	Asn	Thr	Val	Ser	Leu	Ala	Pro	Ala	Ala	Thr		
			660					665					670				
Ser	Ser	Ser	Ser	Thr	Gly	Leu	Gln	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ser		
		675					680					685					
Asn	Leu	Ala	Thr	Thr	Ala	Ala	Leu	Lys	Ser	Ala	Glu	Lys	Lys	Ala			
	690					695						700					
Glu	Ala	Pro	Thr	Ile	Thr	Pro	Phe	Ser	Phe	Gly	Lys	Thr	Asp	Gln	Asn		
705					710					715					720		
Lys	Glu	Thr	Ala	Ser	Thr	Ser	Phe	Val	Phe	Gly	Lys	Lys	Asp	Glu	Lys		
				725					730					735			

Thr Asp Ser Ala Pro Thr Gly Ser Ser Phe Ala Phe Gly Leu Lys Lys  
 740 745 750  
 Asp Gly Glu Glu Ser Lys Pro Phe Leu Phe Gly Lys Pro Glu Pro Thr  
 755 760 765  
 Lys Val Asp Gly Asn Ala Ala Ser Ala Gly Phe Ala Phe Gly Val Thr  
 770 775 780  
 Asn Pro Thr Glu Lys Lys Asp Ile Glu Gln Pro Gly Lys Ser Val Phe  
 785 790 795 800  
 Ala Phe Gly Ala Gln Thr Ser Ile Thr Asp Ala Gly Ala Ser Lys Gln  
 805 810 815  
 Pro Phe Ser Phe Leu Thr Asn Val Ser Ser Thr Ala Ala Ser Ser Ser  
 820 825 830  
 Thr Cys Gly Val Ser Ser Ser Val Phe Gly Ser Val Thr Gln Ser Ser  
 835 840 845  
 Thr Pro Ala Thr Pro Ser Asn Val Phe Gly Ser Ala Ile Ser Ala Asn  
 850 855 860  
 Ala Pro Ala Pro Ser Ser Gly Val Phe Gly Asn Leu Thr Pro Ser Asn  
 865 870 875 880  
 Ala Pro Ala Ala Ser Ser Thr Leu Phe Gly Asn Val Ala Pro Ser Ser  
 885 890 895  
 Thr Pro Ser Gly Ser Ser Gly Leu Phe Gly Thr Ala Ala Ala Ser Ser  
 900 905 910  
 Thr Pro Ala Thr Ser Thr Ser Leu Phe Gly Ser Ala Ala Lys Ser Ser  
 915 920 925  
 Ala Pro Ala Ser Ser Gly Gly Val Phe Asn Ser Ala Ala Pro Ala Ala  
 930 935 940  
 Pro Ala Ser Thr Thr Ser Ser Val Phe Gly Ser Val Ala Ser Ser Thr  
 945 950 955 960  
 Asn Thr Ser Ala Asn Ser Ala Asn Ile Phe Gly Ser Ser Gly Gly Ala  
 965 970 975  
 Ala Thr Ala Pro Gly Ala Phe Val Phe Gly Gln Pro Ala Ser Thr Ala  
 980 985 990  
 Ser Thr Val Phe Gly Asn Ser Ser Glu Ser Lys Ser Thr Phe Val Phe  
 995 1000 1005  
 Ser Gly Gln Glu Asn Lys Pro Val Thr Ser Ala Ser Thr Ser Val Thr  
 1010 1015 1020  
 Pro Phe Leu Phe Gly Ala Val Ser Ala Thr Thr Pro Ala Ala Pro  
 1025 1030 1035 1040  
 Ser Phe Asn Phe Gly Arg Thr Ile Thr Ser Asn Thr Thr Gly Thr Ser  
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 Ser Ser Pro Phe Ile Phe Gly Ala Gly Ala Ser Gly Ser Ala Ser Ser  
 1060 1065 1070  
 Ser Ile Thr Ala Gln Ala Asn Pro Val Pro Ala Phe Gly Gln Ser Ser  
 1075 1080 1085  
 Asn Pro Ser Thr Ala Pro Ala Phe Gly Ser Ser Thr Ser Val Pro Val  
 1090 1095 1100  
 Phe Pro Ala Gly Ser Ser Gln Gln Val Pro Ala Phe Gly Ser Ser Ser  
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 Ala Gln Pro Pro Val Phe Gly Gln Gln Ala Ala Gln Pro Ser Phe Gly  
 1125 1130 1135  
 Ser Pro Ala Ala Pro Ser Ala Gly Ser Gly Phe Pro Phe Gly Asn Asn  
 1140 1145 1150  
 Ala Asn Phe Asn Phe Asn Ser Thr Asn Ser Ser Gly Gly Val Phe Thr  
 1155 1160 1165  
 Phe Asn Ala Asn Ser Gly Ser Thr Thr Gln Pro Pro Pro Gly Tyr  
 1170 1175 1180  
 Met Phe Asn Ala Ala Ala Pro Gly Phe Asn Ile Gly Thr Asn Gly Arg  
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 Thr Thr Pro Ala Ser Thr Ile Ser Thr Arg Lys Ile Lys Thr Ala Arg  
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 Arg Arg Lys

<210> 7  
 <211> 10697  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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 ggcgcgatga ggcgcagcaa ggctgacgtg gagcggtaca tcgcctcggg gcagggctcc 180  
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<211> 3224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
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Thr	Thr	Gln	Pro	Thr	Pro	Phe	Lys	Phe	Asn	Ser	Asn	Phe	Lys	Ser	Asn	
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Asp	Lys	Pro	Leu	Gln	Gly	Asp	Gly	Tyr	Ser	Gly	Ala	Lys	Pro	Ile	Pro	
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 Phe Lys Phe Gly Gln Gly Asp Leu Pro Lys Pro Ile Asn Ser Asp Phe  
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 Thr Thr Ile Lys Pro Asn Pro Glu Asn Thr Gly Pro Thr Leu Glu Trp  
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 Leu Phe Arg Phe Gly Glu Ser Thr Thr Gly Phe Asn Phe Ser Phe Lys  
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 2340 2345 2350  
 Gly Ile Gly Asp Ile Lys Ile Leu Gln Asn Tyr Asp Asn Lys Gln Val  
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 2385 2390 2395 2400  
 Val Trp Leu Trp Thr Ala Cys Asp Phe Ala Asp Gly Glu Arg Lys Val  
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 Glu His Leu Ala Val Arg Phe Lys Leu Gln Asp Val Ala Asp Ser Phe  
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 Lys Lys Ile Phe Asp Glu Ala Lys Thr Ala Gln Glu Lys Asp Ser Leu  
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 Val Lys Asn Leu Phe Ala Ser Phe Pro Thr Glu Glu Ser Ser Ile Asn  
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 Tyr Thr Phe Lys Thr Pro Glu Lys Ala Lys Glu Lys Lys Pro Glu  
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 2740 2745 2750  
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 Thr Gly Pro Gly Leu Leu Ser Met Ala Asn Gln Gly Gln Asn Thr Asn  
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 Asn Ser Gln Phe Val Ile Thr Leu Lys Lys Ala Glu His Leu Asp Phe  
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 Lys His Val Val Phe Gly Phe Val Lys Asp Gly Met Asp Thr Val Lys  
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Lys Ile Glu Ser Phe Gly Ser Pro Lys Gly Ser Val Cys Arg Arg Ile  
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&lt;210&gt; 9

&lt;211&gt; 4346

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
       synthetic construct

&lt;400&gt; 9

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<210> 10

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 10

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          35           40           45
Asn Arg Asn Lys Thr Gly Glu Ile Thr Ala Ser Ser Asn Lys Ser Leu
          50           55           60
Asn Leu Leu Lys Ile Lys His Gly Asp Leu Leu Phe Leu Phe Pro Ser
          65           70           75           80
Ser Leu Ala Gly Pro Ser Ser Glu Met Glu Thr Ser Val Pro Pro Gly
          85           90           95
Phe Lys Val Phe Gly Ala Pro Asn Val Val Glu Asp Glu Ile Asp Gln
          100          105          110
Tyr Leu Ser Lys Gln Asp Gly Lys Ile Tyr Arg Ser Arg Asp Pro Gln
          115          120          125
Leu Cys Arg His Gly Pro Leu Gly Lys Cys Val His Cys Val Pro Leu
          130          135          140
Glu Pro Phe Asp Glu Asp Tyr Leu Asn His Leu Glu Pro Pro Val Lys
          145          150          155          160
His Met Ser Phe His Ala Tyr Ile Arg Lys Leu Thr Gly Gly Ala Asp
          165          170          175

```

Lys	Gly	Lys	Phe	Val	Ala	Leu	Glu	Asn	Ile	Ser	Cys	Lys	Ile	Lys	Ser	180	185	190
Gly	Cys	Glu	Gly	His	Leu	Pro	Trp	Pro	Asn	Gly	Ile	Cys	Thr	Lys	Cys	195	200	205
Gln	Pro	Ser	Ala	Ile	Thr	Leu	Asn	Arg	Gln	Lys	Tyr	Arg	His	Val	Asp	210	215	220
Asn	Ile	Met	Phe	Glu	Asn	His	Thr	Val	Ala	Asp	Arg	Phe	Leu	Asp	Phe	225	230	235
Trp	Arg	Lys	Thr	Gly	Asn	Gln	Gln	Phe	Gly	Tyr	Leu	Tyr	Gly	Arg	Tyr	245	250	255
Thr	Glu	His	Lys	Asp	Ile	Pro	Leu	Gly	Ile	Arg	Ala	Glu	Val	Ala	Ala	260	265	270
Ile	Tyr	Glu	Pro	Pro	Gln	Ile	Gly	Thr	Gln	Asn	Ser	Leu	Glu	Leu	Leu	275	280	285
Glu	Asp	Pro	Lys	Ala	Glu	Val	Val	Asp	Glu	Ile	Ala	Ala	Lys	Leu	Gly	290	295	300
Leu	Arg	Lys	Val	Gly	Trp	Ile	Phe	Thr	Asp	Leu	Val	Ser	Glu	Asp	Thr	305	310	315
Arg	Lys	Gly	Thr	Val	Arg	Tyr	Ser	Arg	Asn	Lys	Asp	Thr	Tyr	Phe	Leu	325	330	335
Ser	Ser	Glu	Glu	Cys	Ile	Thr	Ala	Gly	Asp	Phe	Gln	Asn	Lys	His	Pro	340	345	350
Asn	Met	Cys	Arg	Leu	Ser	Pro	Asp	Gly	His	Phe	Gly	Ser	Lys	Phe	Val	355	360	365
Thr	Ala	Val	Ala	Thr	Gly	Gly	Pro	Asp	Asn	Gln	Val	His	Phe	Glu	Gly	370	375	380
Tyr	Gln	Val	Ser	Asn	Gln	Cys	Met	Ala	Leu	Val	Arg	Asp	Glu	Cys	Leu	385	390	395
Leu	Pro	Cys	Lys	Asp	Ala	Pro	Glu	Leu	Gly	Tyr	Ala	Lys	Glu	Ser	Ser	405	410	415
Ser	Glu	Gln	Tyr	Val	Pro	Asp	Val	Phe	Tyr	Lys	Asp	Val	Asp	Lys	Phe	420	425	430
Gly	Asn	Glu	Ile	Thr	Gln	Leu	Ala	Arg	Pro	Leu	Pro	Val	Glu	Tyr	Leu	435	440	445
Ile	Ile	Asp	Ile	Thr	Thr	Thr	Phe	Pro	Lys	Asp	Pro	Val	Tyr	Thr	Phe	450	455	460
Ser	Ile	Ser	Gln	Asn	Pro	Phe	Pro	Ile	Glu	Asn	Arg	Asp	Val	Leu	Gly	465	470	475
Glu	Thr	Gln	Asp	Phe	His	Ser	Leu	Ala	Thr	Tyr	Leu	Ser	Gln	Asn	Thr	485	490	495
Ser	Ser	Val	Phe	Leu	Asp	Thr	Ile	Ser	Asp	Phe	His	Leu	Leu	Leu	Phe	500	505	510
Leu	Val	Thr	Asn	Glu	Val	Met	Pro	Leu	Gln	Asp	Ser	Ile	Ser	Leu	Leu	515	520	525
Leu	Glu	Ala	Val	Arg	Thr	Arg	Asn	Glu	Glu	Leu	Ala	Gln	Thr	Trp	Lys	530	535	540
Arg	Ser	Glu	Gln	Trp	Ala	Thr	Ile	Glu	Gln	Leu	Cys	Ser	Thr	Val	Gly	545	550	555
Gly	Gln	Leu	Pro	Gly	Leu	His	Glu	Tyr	Gly	Ala	Val	Glu	Gly	Ser	Thr	565	570	575
His	Thr	Ala	Thr	Ala	Ala	Met	Trp	Ala	Cys	Gln	His	Cys	Thr	Phe	Met	580	585	590
Asn	Gln	Pro	Gly	Thr	Gly	His	Cys	Glu	Met	Cys	Ser	Leu	Pro	Arg	Thr	595	600	605

&lt;210&gt; 11

&lt;211&gt; 3067

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 11

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ggtgggttta tctcaaggcc tgagtagccg gtaacaaacg agggttcccg ggattggacc      60
gacgcaccat gcctctgcga cttgatatca aaagaaagct aactgctaga tctgatcgag      120
ttaagagtgt ggatctgcat cctacagagc catggatgtt ggcaagtctt tacaatggca      180
gtgtgtgtgt ttggaatcat gaaacacaga cactggtgaa gacatttgaa gtatgtgac      240
ttcctgttcg agctgcaaag tttgttgcaa ggaagaattg ggttgtgaca ggagcggatg      300
acatgcagat tagagtgttc aattacaata ctctggagag agttcatatg tttgaagcac      360
actcagacta cattcgctgt attgctgttc atccaaccca gcctttcatt ctaactagca      420
gtgatgacat gcttattaag ctctgggact gggataaaaa atggtcttgc tcacaagtgt      480
ttgaaggaca caccattat gttatgcaga ttgtgatcaa ccccaaagat aacaatcagt      540
ttgccagtgc ctctttggac aggactatca aggtgtggca gttgggctct tcgtcaccaa      600
acttcacttt ggaaggacat gagaaaggcg tgaattgcat tgattactac agtgggtggg      660
acaagccata cctcatttca ggtgcagatg accgtcttgt taaaatatgg gattatcaga      720
ataaaacatg tgtgcagaca ctggaaggac atgcccacaa tgtgtcttgt gccagctttc      780
atcctgagtt gccaatcatt atcacagggt cagaagatgg aacagtacgt atttggcatt      840
caagcaccta ccggtctgag agcacactga attatggaat ggagagggtg tgggtgcgtg      900
ccagtctaag aggggtcaaac aatgtcgctt tgggctatga tgaaggagag atcattgtta      960
agcttggctg ggaggaaacct gccatgtcca tggatgcaa tggaaagata atttgggcca      1020
agcattcaga agtccagcag gccaacctaa aagcaatggg agatgctgaa attaaagatg      1080
gtgaaagatt gccactggca gtaaaggata tgggcagtgt tgaaatatac cctcagacta      1140
ttcagcacia tcctaattgg cggtttgtgg tgggtgtgtg tgatggggag tatatcatct      1200
acacagcaat ggcattgaga aacaagagct ttggatctgc tcaggagttt gcatggggcc      1260
acgattcttc agagtatgca ataagagaga gcaacagcat tgtaaagata tttaagaact      1320
ttaaggaaaa aaaatcattt aaaccagatt ttggagcaga aagtatctac ggcggtcttct      1380
tattgggagt cagatctgta aatggcttag ccttctatga ctgggacaat acagaactca      1440
tacgaagaat tgaaattcag cccaaacata ttttctggtc tgactctgga gagctagtct      1500
gtattgtctac tgaggaatca ttttttatcc ttaagtatct gtcagaaaaa gtcttgctg      1560
cacaggaaac acatgaggga gttactgaag atggcattga agatgccttt gaggttcttg      1620
gtgagattca ggaaattgtg aaaacagggc tttgggtagg cgattgcttc atttacacaa      1680
gttctgtgaa cagattaaat tattatgttg gaggagaaat agtcaccatt gccacttgg      1740
acaggacgat gtatctccta ggctacattc ctaaagacaa caggctttat ctgggggata      1800
aagaattgaa catcattagc tattccctgc tggtttcagt cctggaatac cagacagctg      1860
tcatgcggag ggacttttagc atggctgata aggtccttcc taccattcca aaagaacaga      1920
ggaccagagt tgcacacttt ttggaaaagc agggcttcaa gcagcaagct cttacagtat      1980
ccacagatcc tgagcatcgt tttgagcttg ctcttcagct tggagagtta aaaattgcat      2040
accagttagc agtggaagca gagtgcgaac agaagtggaa acaacttgct gaacttgcca      2100
ttagtaaatg tcagtttggc ctagcccagg agtgcctgca tcatgcacag gattatgggg      2160
gcctgctgct tttggccact gcctctggaa atgctaatat ggtgaacaag ctagcagagg      2220
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ttgatgcctg cctagagctc ttaattagaa ctggacggct gccagaagct gccttcttgg      2340
cccgaactta cttaccagat caggtttcaa gggtagtgaa actctggaga gagaatctct      2400
caaaagtcaa tcagaaagca gcagaatccc ttgctgaccc aacagagtat gaaaacctgt      2460
tccttgattt aaaagaagcc tttgttgttg aagaatgggt gaaggaaaca catgctgatc      2520
tgtggccagc caaacaatac ccacttgta cgccaaatga agagagaaat gtcatggaag      2580
agggaaaaga ctttcagccc tcaagatcta cagctcaaca ggaacttgat gggaacctg      2640
cttctcctac tccggttatt gtggcctccc acacagccaa caaagaagaa aagagtttac      2700
tcgaactaga agtagatttg gataatttgg aattagaaga tattgacaca acagatatca      2760
atctggatga agatattttg gatgattgac tgtaatgctt tccatttacc tgactaaaca      2820
gatcattatt atatataggt attgattgct accctgacca cagtgccttg gactatgaga      2880
aacttcttag atttttatat gtaaagtctg tggaccactg ggagcacaat gccacatca      2940
tcttaagaag agtttatgtg cagcatttaa atcactgtgt tttccttgtt aactaaaaca      3000
gacatgggct ttgatttttt tcatactatt agaccatata tcataaaacc ttttgaatta      3060
aaaaaaa

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<210> 12

<211> 906

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 12

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Arg	Val	Lys	Ser	Val	Asp	Leu	His	Pro	Thr	Glu	Pro	Trp	Met	Leu	Ala
		20						25					30		
Ser	Leu	Tyr	Asn	Gly	Ser	Val	Cys	Val	Trp	Asn	His	Glu	Thr	Gln	Thr
	35						40					45			
Leu	Val	Lys	Thr	Phe	Glu	Val	Cys	Asp	Leu	Pro	Val	Arg	Ala	Ala	Lys
	50					55					60				
Phe	Val	Ala	Arg	Lys	Asn	Trp	Val	Val	Thr	Gly	Ala	Asp	Asp	Met	Gln
65					70					75					80
Ile	Arg	Val	Phe	Asn	Tyr	Asn	Thr	Leu	Glu	Arg	Val	His	Met	Phe	Glu
			85					90						95	
Ala	His	Ser	Asp	Tyr	Ile	Arg	Cys	Ile	Ala	Val	His	Pro	Thr	Gln	Pro
			100					105						110	
Phe	Ile	Leu	Thr	Ser	Ser	Asp	Asp	Met	Leu	Ile	Lys	Leu	Trp	Asp	Trp
		115					120					125			
Asp	Lys	Lys	Trp	Ser	Cys	Ser	Gln	Val	Phe	Glu	Gly	His	Thr	His	Tyr
	130					135					140				
Val	Met	Gln	Ile	Val	Ile	Asn	Pro	Lys	Asp	Asn	Asn	Gln	Phe	Ala	Ser
145					150					155					160
Ala	Ser	Leu	Asp	Arg	Thr	Ile	Lys	Val	Trp	Gln	Leu	Gly	Ser	Ser	Ser
			165					170						175	
Pro	Asn	Phe	Thr	Leu	Glu	Gly	His	Glu	Lys	Gly	Val	Asn	Cys	Ile	Asp
		180						185					190		
Tyr	Tyr	Ser	Gly	Gly	Asp	Lys	Pro	Tyr	Leu	Ile	Ser	Gly	Ala	Asp	Asp
		195					200					205			
Arg	Leu	Val	Lys	Ile	Trp	Asp	Tyr	Gln	Asn	Lys	Thr	Cys	Val	Gln	Thr
	210					215					220				
Leu	Glu	Gly	His	Ala	Gln	Asn	Val	Ser	Cys	Ala	Ser	Phe	His	Pro	Glu
225					230					235					240
Leu	Pro	Ile	Ile	Ile	Thr	Gly	Ser	Glu	Asp	Gly	Thr	Val	Arg	Ile	Trp
			245						250					255	
His	Ser	Ser	Thr	Tyr	Arg	Leu	Glu	Ser	Thr	Leu	Asn	Tyr	Gly	Met	Glu
			260					265					270		
Arg	Val	Trp	Cys	Val	Ala	Ser	Leu	Arg	Gly	Ser	Asn	Asn	Val	Ala	Leu
		275					280					285			
Gly	Tyr	Asp	Glu	Gly	Ser	Ile	Ile	Val	Lys	Leu	Gly	Arg	Glu	Glu	Pro
	290					295					300				
Ala	Met	Ser	Met	Asp	Ala	Asn	Gly	Lys	Ile	Ile	Trp	Ala	Lys	His	Ser
305					310					315					320
Glu	Val	Gln	Gln	Ala	Asn	Leu	Lys	Ala	Met	Gly	Asp	Ala	Glu	Ile	Lys
			325						330					335	
Asp	Gly	Glu	Arg	Leu	Pro	Leu	Ala	Val	Lys	Asp	Met	Gly	Ser	Cys	Glu
		340					345					350			
Ile	Tyr	Pro	Gln	Thr	Ile	Gln	His	Asn	Pro	Asn	Gly	Arg	Phe	Val	Val
		355					360					365			
Val	Cys	Gly	Asp	Gly	Glu	Tyr	Ile	Ile	Tyr	Thr	Ala	Met	Ala	Leu	Arg
	370					375					380				
Asn	Lys	Ser	Phe	Gly	Ser	Ala	Gln	Glu	Phe	Ala	Trp	Ala	His	Asp	Ser
385					390					395					400
Ser	Glu	Tyr	Ala	Ile	Arg	Glu	Ser	Asn	Ser	Ile	Val	Lys	Ile	Phe	Lys
			405						410					415	
Asn	Phe	Lys	Glu	Lys	Lys	Ser	Phe	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ser
		420						425					430		

Ile	Tyr	Gly	Gly	Phe	Leu	Leu	Gly	Val	Arg	Ser	Val	Asn	Gly	Leu	Ala	435	440	445
Phe	Tyr	Asp	Trp	Asp	Asn	Thr	Glu	Leu	Ile	Arg	Arg	Ile	Glu	Ile	Gln	450	455	460
Pro	Lys	His	Ile	Phe	Trp	Ser	Asp	Ser	Gly	Glu	Leu	Val	Cys	Ile	Ala	465	470	475
Thr	Glu	Glu	Ser	Phe	Phe	Ile	Leu	Lys	Tyr	Leu	Ser	Glu	Lys	Val	Leu	485	490	495
Ala	Ala	Gln	Glu	Thr	His	Glu	Gly	Val	Thr	Glu	Asp	Gly	Ile	Glu	Asp	500	505	510
Ala	Phe	Glu	Val	Leu	Gly	Glu	Ile	Gln	Glu	Ile	Val	Lys	Thr	Gly	Leu	515	520	525
Trp	Val	Gly	Asp	Cys	Phe	Ile	Tyr	Thr	Ser	Ser	Val	Asn	Arg	Leu	Asn	530	535	540
Tyr	Tyr	Val	Gly	Gly	Glu	Ile	Val	Thr	Ile	Ala	His	Leu	Asp	Arg	Thr	545	550	555
Met	Tyr	Leu	Leu	Gly	Tyr	Ile	Pro	Lys	Asp	Asn	Arg	Leu	Tyr	Leu	Gly	565	570	575
Asp	Lys	Glu	Leu	Asn	Ile	Ile	Ser	Tyr	Ser	Leu	Leu	Val	Ser	Val	Leu	580	585	590
Glu	Tyr	Gln	Thr	Ala	Val	Met	Arg	Arg	Asp	Phe	Ser	Met	Ala	Asp	Lys	595	600	605
Val	Leu	Pro	Thr	Ile	Pro	Lys	Glu	Gln	Arg	Thr	Arg	Val	Ala	His	Phe	610	615	620
Leu	Glu	Lys	Gln	Gly	Phe	Lys	Gln	Gln	Ala	Leu	Thr	Val	Ser	Thr	Asp	625	630	635
Pro	Glu	His	Arg	Phe	Glu	Leu	Ala	Leu	Gln	Leu	Gly	Glu	Leu	Lys	Ile	645	650	655
Ala	Tyr	Gln	Leu	Ala	Val	Glu	Ala	Glu	Ser	Glu	Gln	Lys	Trp	Lys	Gln	660	665	670
Leu	Ala	Glu	Leu	Ala	Ile	Ser	Lys	Cys	Gln	Phe	Gly	Leu	Ala	Gln	Glu	675	680	685
Cys	Leu	His	His	Ala	Gln	Asp	Tyr	Gly	Gly	Leu	Leu	Leu	Leu	Ala	Thr	690	695	700
Ala	Ser	Gly	Asn	Ala	Asn	Met	Val	Asn	Lys	Leu	Ala	Glu	Gly	Ala	Glu	705	710	715
Arg	Asp	Gly	Lys	Asn	Asn	Val	Ala	Phe	Met	Ser	Tyr	Phe	Leu	Gln	Gly	725	730	735
Lys	Val	Asp	Ala	Cys	Leu	Glu	Leu	Leu	Ile	Arg	Thr	Gly	Arg	Leu	Pro	740	745	750
Glu	Ala	Ala	Phe	Leu	Ala	Arg	Thr	Tyr	Leu	Pro	Ser	Gln	Val	Ser	Arg	755	760	765
Val	Val	Lys	Leu	Trp	Arg	Glu	Asn	Leu	Ser	Lys	Val	Asn	Gln	Lys	Ala	770	775	780
Ala	Glu	Ser	Leu	Ala	Asp	Pro	Thr	Glu	Tyr	Glu	Asn	Leu	Phe	Pro	Gly	785	790	795
Leu	Lys	Glu	Ala	Phe	Val	Val	Glu	Glu	Trp	Val	Lys	Glu	Thr	His	Ala	805	810	815
Asp	Leu	Trp	Pro	Ala	Lys	Gln	Tyr	Pro	Leu	Val	Thr	Pro	Asn	Glu	Glu	820	825	830
Arg	Asn	Val	Met	Glu	Glu	Gly	Lys	Asp	Phe	Gln	Pro	Ser	Arg	Ser	Thr	835	840	845
Ala	Gln	Gln	Glu	Leu	Asp	Gly	Lys	Pro	Ala	Ser	Pro	Thr	Pro	Val	Ile	850	855	860
Val	Ala	Ser	His	Thr	Ala	Asn	Lys	Glu	Glu	Lys	Ser	Leu	Leu	Glu	Leu	865	870	875
Glu	Val	Asp	Leu	Asp	Asn	Leu	Glu	Leu	Glu	Asp	Ile	Asp	Thr	Thr	Asp	885	890	895
Ile	Asn	Leu	Asp	Glu	Asp	Ile	Leu	Asp	Asp							900	905	

<210> 13  
 <211> 914  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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<400> 13
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gcggttcgag gaaccttccc tctacaccat caaggctgtt ttcatacctag ataatgacgg      180
gcgcccggctg ctggccaagt attatgatga cacattcccc tccatgaagg agcagatggg      240
tttcgagaaa aatgtcttca acaagaccag ccggactgag agtgagattg catttttttg      300
gggtatgacc atcgtctaca agaacagcat tgacctcttc ctatacgtgg tgggctcatc      360
ctacgagaat gagctgatgc tcatgtctgt tctcacctgc ctgtttgagt ctctgaacca      420
catgttaagg aagaacgtgg agaagcgtg gttgctggag aacatggacg gagccttctt      480
ggtgctggac gagattgtgg atggcggtgt gattctggag agtgaccccc agcaagtgat      540
ccagaaggtg aatttttagg cagatgatgg cggcttgact gaacagagtg tggcccaggt      600
tcttcagttc gccaaaggaac aaattaaatg gtcgttattg aaatgaaggc tgtggattca      660
aggctccctg cccccagac catttcccca atcctggcaa aagcccaaag atcccagggt      720
caggagagac ccctctgtat cccaggtcc ctcccagaac tgactcctaa ggtctccagc      780
cagggcttct gagatgcaaa ggtttgccct caggagagtc accttttctc acggccctgg      840
ccttaactca tatcttaggc attcctggcc ccagggccct aataaacctg cttttgtctt      900
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<210> 14  
 <211> 210  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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<400> 14
Met Gln Arg Pro Glu Ala Trp Pro Arg Pro His Pro Gly Glu Gly Ala
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Ala Ala Ala Gln Ala Gly Gly Pro Ala Pro Pro Ala Arg Ala Gly Glu
20          25          30
Pro Ser Gly Leu Arg Leu Gln Glu Pro Ser Leu Tyr Thr Ile Lys Ala
35          40          45
Val Phe Ile Leu Asp Asn Asp Gly Arg Arg Leu Leu Ala Lys Tyr Tyr
50          55          60
Asp Asp Thr Phe Pro Ser Met Lys Glu Gln Met Val Phe Glu Lys Asn
65          70          75          80
Val Phe Asn Lys Thr Ser Arg Thr Glu Ser Glu Ile Ala Phe Phe Gly
85          90          95
Gly Met Thr Ile Val Tyr Lys Asn Ser Ile Asp Leu Phe Leu Tyr Val
100         105         110
Val Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ser Val Leu Thr
115         120         125
Cys Leu Phe Glu Ser Leu Asn His Met Leu Arg Lys Asn Val Glu Lys
130         135         140
Arg Trp Leu Leu Glu Asn Met Asp Gly Ala Phe Leu Val Leu Asp Glu
145         150         155         160
Ile Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Ile
165         170         175
Gln Lys Val Asn Phe Arg Ala Asp Asp Gly Gly Leu Thr Glu Gln Ser
180         185         190
```

## ATTORNEY DOCKET 21101.0045U2

Val Ala Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu  
 195 200 205  
 Leu Lys  
 210

&lt;210&gt; 15

&lt;211&gt; 5064

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 15

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agaggattta	caggggtggg	ggacagaggg	gcagcaggaa	ccagaagggg	gacagtggcg	120
gtcgcaccgg	ggccgatccg	agagttcccc	ttagagaacg	gagctcacgg	gcggggaggc	180
ctcacctgct	agtaggacgc	agaaagacag	aaggcgaagg	agacccccctg	ccgtagccat	240
cttgccctctc	tgctgagcgg	aagcccccg	tcggctcctg	tctgttagcg	gcctctctag	300
gctaccactg	acaccgtctc	tgtggcccgg	agcctaagag	accggaagtt	cgtgtttcca	360
ggcgcttccg	gaaaccgcgg	gagagggtcg	ctgacgtgga	ggcgccgaa	gggcagcagg	420
gtgtgtcggg	gctcggatta	agacatcgga	gtcggagacc	tgagagatgt	taaccaaatt	480
cgagaccaag	agcgcgcggg	tcaaagggct	cagctttcac	cccaaaagac	cttggatcct	540
gactagttta	cataatgggg	tcatccagtt	atgggactat	cggatgtgca	ctctcattga	600
caagtttgat	gaacatgatg	gtccagtgcg	aggcattgac	ttccataagc	agcagccact	660
gttcgtctct	ggaggagatg	actataagat	taaggtttgg	aattacaagc	ttcggcgctg	720
tcttttcaca	ttgcttgggc	acttagatta	tattcgcacc	acgttttttc	atcatgaata	780
tccttggtat	tcgagtgcct	ccgatgatca	gaccatccga	gtgtggaatt	ggcaatctag	840
aacctgtggt	tgtgtgtaaa	cagggcacaa	ccattatgtg	atgtgtgctc	agttccaccc	900
cacagaagac	ttggtagtat	cagccagcct	ggaccagact	gtgcgcgttt	gggatatttc	960
tgggtctgagg	aaaaaaaaacc	tgtccctggg	tgcggtggaa	tcggatgtga	gaggaataac	1020
tgggggttgat	ctatttgga	ctacagatgc	agtgggtgaag	catgtactag	agggtcacga	1080
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<210> 16

<211> 1224

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 16

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Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val
      20             25             30
Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp
      35             40             45
Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
      50             55             60
Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
65             70             75             80

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Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile  
 85 90 95  
 Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser  
 100 105 110  
 Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val  
 115 120 125  
 Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His  
 130 135 140  
 Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg  
 145 150 155 160  
 Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala  
 165 170 175  
 Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr  
 180 185 190  
 Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val  
 195 200 205  
 Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala  
 210 215 220  
 Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp  
 225 230 235 240  
 Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val  
 245 250 255  
 Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser  
 260 265 270  
 Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg  
 275 280 285  
 Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn  
 290 295 300  
 Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu  
 305 310 315 320  
 Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val  
 325 330 335  
 Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val  
 340 345 350  
 Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met  
 355 360 365  
 Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser  
 370 375 380  
 Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys Asp Ala  
 385 390 395 400  
 Asp Ser Gln Asn Pro Asp Ala Pro Glu Gly Lys Arg Ser Ser Gly Leu  
 405 410 415  
 Thr Ala Val Trp Val Ala Arg Asn Arg Phe Ala Val Leu Asp Arg Met  
 420 425 430  
 His Ser Leu Leu Ile Lys Asn Leu Lys Asn Glu Ile Thr Lys Lys Val  
 435 440 445  
 Gln Val Pro Asn Cys Asp Glu Ile Phe Tyr Ala Gly Thr Gly Asn Leu  
 450 455 460  
 Leu Leu Arg Asp Ala Asp Ser Ile Thr Leu Phe Asp Val Gln Gln Lys  
 465 470 475 480  
 Arg Thr Leu Ala Ser Val Lys Ile Ser Lys Val Lys Tyr Val Ile Trp  
 485 490 495  
 Ser Ala Asp Met Ser His Val Ala Leu Leu Ala Lys His Ala Ile Val  
 500 505 510  
 Ile Cys Asn Arg Lys Leu Asp Ala Leu Cys Asn Ile His Glu Asn Ile  
 515 520 525  
 Arg Val Lys Ser Gly Ala Trp Asp Glu Ser Gly Val Phe Ile Tyr Thr  
 530 535 540  
 Thr Ser Asn His Ile Lys Tyr Ala Val Thr Thr Gly Asp His Gly Ile  
 545 550 555 560

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Ile Arg Thr Leu Asp Leu Pro Ile Tyr Val Thr Arg Val Lys Gly Asn
565 570 575
Asn Val Tyr Cys Leu Asp Arg Glu Cys Arg Pro Arg Val Leu Thr Ile
580 585 590
Asp Pro Thr Glu Phe Lys Phe Lys Leu Ala Leu Ile Asn Arg Lys Tyr
595 600 605
Asp Glu Val Leu His Met Val Arg Asn Ala Lys Leu Val Gly Gln Ser
610 615 620
Ile Ile Ala Tyr Leu Gln Lys Lys Gly Tyr Pro Glu Val Ala Leu His
625 630 635 640
Phe Val Lys Asp Glu Lys Thr Arg Phe Ser Leu Ala Leu Glu Cys Gly
645 650 655
Asn Ile Glu Ile Ala Leu Glu Ala Ala Lys Ala Leu Asp Asp Lys Asn
660 665 670
Cys Trp Glu Lys Leu Gly Glu Val Ala Leu Leu Gln Gly Asn His Gln
675 680 685
Ile Val Glu Met Cys Tyr Gln Arg Thr Lys Asn Phe Asp Lys Val Ser
690 695 700
Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys Leu Arg Lys Met Met
705 710 715 720
Lys Ile Ala Glu Ile Arg Lys Asp Met Ser Gly His Tyr Gln Asn Ala
725 730 735
Leu Tyr Leu Gly Asp Val Ser Glu Arg Val Arg Ile Leu Lys Asn Cys
740 745 750
Gly Gln Lys Ser Leu Ala Tyr Leu Thr Ala Ala Thr His Gly Leu Asp
755 760 765
Glu Glu Ala Glu Ser Leu Lys Glu Thr Phe Asp Pro Glu Lys Glu Thr
770 775 780
Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro
785 790 795 800
Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly
805 810 815
Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala
820 825 830
Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp
835 840 845
Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly
850 855 860
Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Glu Gly Gly Gly Trp
865 870 875 880
Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro
885 890 895
Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys
900 905 910
Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val
915 920 925
Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His
930 935 940
Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu
945 950 955 960
Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu
965 970 975
Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu
980 985 990
Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln
995 1000 1005
Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu Glu
1010 1015 1020
Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu Leu Val
1025 1030 1035 1040

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Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu Ile Thr Ile  
1045 1050 1055  
Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg Lys Lys  
1060 1065 1070  
Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg Ile Cys Glu Met Ala  
1075 1080 1085  
Ala Tyr Phe Thr His Ser Asn Leu Gln Pro Val His Met Ile Leu Val  
1090 1095 1100  
Leu Arg Thr Ala Leu Asn Leu Phe Phe Lys Leu Lys Asn Phe Lys Thr  
1105 1110 1115 1120  
Ala Ala Thr Phe Ala Arg Arg Leu Leu Glu Leu Gly Pro Lys Pro Glu  
1125 1130 1135  
Val Ala Gln Gln Thr Arg Lys Ile Leu Ser Ala Cys Glu Lys Asn Pro  
1140 1145 1150  
Thr Asp Ala Tyr Gln Leu Asn Tyr Asp Met His Asn Pro Phe Asp Ile  
1155 1160 1165  
Cys Ala Ala Ser Tyr Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys  
1170 1175 1180  
Cys Pro Leu Ser Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile  
1185 1190 1195 1200  
Cys Arg Val Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu  
1205 1210 1215  
Arg Ile Ser Pro Leu Gln Phe Arg  
1220

&lt;210&gt; 17

&lt;211&gt; 1208

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 17

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cataaacgag	gcgcagcggg	tgaagctgtc	aaagcccagag	agagacgtgg	agagggacgt	180
cttcctgtat	agagcgtacc	tggcgcagag	gaagttcggg	gtggctcctgg	atgagatcaa	240
gccctcctcg	gccccctgagc	tccaggccgt	gcgcatgttt	gctgactacc	tcgcccacga	300
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&lt;210&gt; 18

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 18

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Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
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Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
 20           25           30
Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
 35           40           45
Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
 50           55           60
Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
 65           70           75           80
Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
 85           90           95
Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Val
100           105           110
Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
115           120           125
His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
130           135           140
Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
145           150           155           160
Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
165           170           175
Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
180           185           190
Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met
195           200           205
Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala
210           215           220
Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln
225           230           235           240
Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu
245           250           255
Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg
260           265           270
Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys
275           280           285
Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr
290           295           300
Ala Pro Ser Ala
305

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&lt;210&gt; 19

&lt;211&gt; 3528

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 19

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cacaagcccc cagtcccaga ggcgtggtgg gtcgggcaga gtcggaagaa ctggctttct      180
agctggaaga tgcggaaggg gagcgactag gccgcttgcg tctgggcctg gcagaaggga      240

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ccggattttc	tggcatcctt	aaatccttg	tcaaggattg	gttataatat	aaccagaaac	300
catgacggcg	gctgagaacg	tatgctacac	gttaattaac	gtgccaatgg	attcagaacc	360
accatctgaa	attagcttaa	aaaatgatct	agaaaaagga	gatgtaaagt	caaagactga	420
agctttgaag	aaagtaatca	ttatgattct	gaatggtgaa	aaacttcctg	gacttctgat	480
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tgacttcgca	aatattaaag	ctaactgcaa	agtagcatca	acagaaaatg	gaataatttt	2700
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tgatattcac	atcgacatca	tggactatat	ccagcctgca	acttgcaactg	atgcagaatt	2820
ccgtcagatg	tgggcccgaat	ttgaatggga	aaacaaagtg	acagttaaca	ccaacatggt	2880
tgattttaat	gactacttac	agcacatatt	aaagtcaacc	aatatgaaat	gcctgactcc	2940
agaaaaggcc	ctttctggtt	actgtggctt	tatggcagcc	aacctttatg	ctcgttccat	3000
atttggtgaa	gatgcacttg	caaatgtcag	cattgagaag	ccaattcacc	agggaccaga	3060
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acagatctat	tcataaaattt	ttgttatttt	ataaataaat	gattacataa	tttttagttat	3480
aaaaaaaaaa	aaaaaaaaaa	agaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		3528

&lt;210&gt; 20

&lt;211&gt; 953

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<400> 20

36

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Tyr	Cys	Ser	Thr	Lys	Glu	Asp	Ile	Gln	Ser	Val	Met	Thr	Glu	Ile	Arg
465					470					475					480
Arg	Ser	Leu	Gly	Glu	Ile	Pro	Ile	Val	Glu	Ser	Glu	Ile	Lys	Lys	Glu
				485					490					495	
Ala	Gly	Glu	Leu	Lys	Pro	Glu	Glu	Glu	Ile	Thr	Val	Gly	Pro	Val	Gln
			500					505					510		
Lys	Leu	Val	Thr	Glu	Met	Gly	Thr	Tyr	Ala	Thr	Gln	Ser	Ala	Leu	Ser
		515					520					525			
Ser	Ser	Arg	Pro	Thr	Lys	Lys	Glu	Glu	Asp	Arg	Pro	Pro	Leu	Arg	Gly
		530				535					540				
Phe	Leu	Leu	Asp	Gly	Asp	Phe	Phe	Val	Ala	Ala	Ser	Leu	Ala	Thr	Thr
545				550						555					560
Leu	Thr	Lys	Ile	Ala	Leu	Arg	Tyr	Val	Ala	Leu	Val	Gln	Glu	Lys	Lys
				565					570					575	
Lys	Gln	Asn	Ser	Phe	Val	Ala	Glu	Ala	Met	Leu	Leu	Met	Ala	Thr	Ile
			580					585					590		
Leu	His	Leu	Gly	Lys	Ser	Ser	Leu	Pro	Lys	Lys	Pro	Ile	Thr	Asp	Asp
		595					600					605			
Asp	Val	Asp	Arg	Ile	Ser	Leu	Cys	Leu	Lys	Val	Leu	Ser	Glu	Cys	Ser
		610				615					620				
Pro	Leu	Met	Asn	Asp	Ile	Phe	Asn	Lys	Glu	Cys	Arg	Gln	Ser	Leu	Ser
625					630					635					640
His	Met	Leu	Ser	Ala	Lys	Leu	Glu	Glu	Glu	Lys	Leu	Ser	Gln	Lys	Lys
				645					650					655	
Glu	Ser	Glu	Lys	Arg	Asn	Val	Thr	Val	Gln	Pro	Asp	Asp	Pro	Ile	Ser
			660					665					670		
Phe	Met	Gln	Leu	Thr	Ala	Lys	Asn	Glu	Met	Asn	Cys	Lys	Glu	Asp	Gln
		675					680					685			
Phe	Gln	Leu	Ser	Leu	Leu	Ala	Ala	Met	Gly	Asn	Thr	Gln	Arg	Lys	Glu
		690				695					700				
Ala	Ala	Asp	Pro	Leu	Ala	Ser	Lys	Leu	Asn	Lys	Val	Thr	Gln	Leu	Thr
705					710					715					720
Gly	Phe	Ser	Asp	Pro	Val	Tyr	Ala	Glu	Ala	Tyr	Val	His	Val	Asn	Gln
				725					730					735	
Tyr	Asp	Ile	Val	Leu	Asp	Val	Leu	Val	Val	Asn	Gln	Thr	Ser	Asp	Thr
			740					745					750		
Leu	Gln	Asn	Cys	Thr	Leu	Glu	Leu	Ala	Thr	Leu	Gly	Asp	Leu	Lys	Leu
		755					760					765			
Val	Glu	Lys	Pro	Ser	Pro	Leu	Thr	Leu	Ala	Pro	His	Asp	Phe	Ala	Asn
		770				775					780				
Ile	Lys	Ala	Asn	Val	Lys	Val	Ala	Ser	Thr	Glu	Asn	Gly	Ile	Ile	Phe
785					790					795					800
Gly	Asn	Ile	Val	Tyr	Asp	Val	Ser	Gly	Ala	Ala	Ser	Asp	Arg	Asn	Cys
				805				810						815	
Val	Val	Leu	Ser	Asp	Ile	His	Ile	Asp	Ile	Met	Asp	Tyr	Ile	Gln	Pro
			820					825					830		
Ala	Thr	Cys	Thr	Asp	Ala	Glu	Phe	Arg	Gln	Met	Trp	Ala	Glu	Phe	Glu
			835				840					845			
Trp	Glu	Asn	Lys	Val	Thr	Val	Asn	Thr	Asn	Met	Val	Asp	Leu	Asn	Asp
						855					860				
Tyr	Leu	Gln	His	Ile	Leu	Lys	Ser	Thr	Asn	Met	Lys	Cys	Leu	Thr	Pro
865					870					875					880
Glu	Lys	Ala	Leu	Ser	Gly	Tyr	Cys	Gly	Phe	Met	Ala	Ala	Asn	Leu	Tyr
				885					890					895	
Ala	Arg	Ser	Ile	Phe	Gly	Glu	Asp	Ala	Leu	Ala	Asn	Val	Ser	Ile	Glu
			900					905					910		
Lys	Pro	Ile	His	Gln	Gly	Pro	Asp	Ala	Ala	Val	Thr	Gly	His	Ile	Arg
			915				920						925		

ATTORNEY DOCKET 21101.0045U2

Ile Arg Ala Lys Ser Gln Gly Met Ala Leu Ser Leu Gly Asp Lys Ile  
 930 935 940  
 Asn Leu Ser Gln Lys Lys Thr Ser Ile  
 945 950

<210> 21  
 <211> 3075  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 21  
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 cccaccgact ccactatggt gaagaaattc gacaagaagg atgaggagtc aggtggaggc 120  
 tccaacccat tccagcacct tgagaagagt gcggtactcc aggaggcccg tgtattttaat 180  
 gaaactccca tcaaccctcg gaaatgtgcc cacatcctca ccaagattct ttatctcata 240  
 aaccaggggg agcacctggg gaccacggaa gcgaccgagg ccttctttgc catgaccaag 300  
 ctctttcagt ccaatgacct cacactccgt cggatgtgct acttgaccat caaggagatg 360  
 tcttgcatgt cagaggatgt catcattgtc accagcagcc taacaaaaga catgactggg 420  
 aaagaagaca actaccgggg cccggccgtg cgagccctct gccagatcac tgatagcacc 480  
 atgctgcagg ctattgagcg ctacatgaaa caagccattg tggacaagggt gccagtgctc 540  
 tccagctctg cctcgtgtc ttcttgcac ctgctgaagt gcagctttga cgtggtcaag 600  
 cgctgggtga atgaggctca ggaggcagca tccagtata acatcatggt ccagtaccac 660  
 gcaactaggg tcctgtacca tgtgcgtaag aatgaccgcc tagccgtcaa taagatgatc 720  
 agcaaggcca caccgcatgg ccttaagtct ccctttgcct actgcatgat gatccgggtg 780  
 gccagcaagc agctggaaga ggaggatggc agccgtgaca gccactgtt tgacttcac 840  
 gagagctgct tgcgcaacaa gcacgagatg gtggtgtatg aagccgcctc ggccattgtc 900  
 aacctgcctg ggtgcagcgc caaggagctg gcccagctg tctcagtgtc ccagctcttc 960  
 tgcagctccc ccaaggccgc cctccgttac gccgccgtcc gcaccctcaa caagggtggc 1020  
 atgaagcacc cgtccgctgt gacagcttgt aatctggatc tggagaacct ggtcacagat 1080  
 tcaaacgcga gcattgccac gctggccatc accaccctcc ttaagacggg cagcgagagc 1140  
 agcatcgacc gcctcatgaa gcagatctcc tccttcatgt cagaaatctc ggatgaattc 1200  
 aagggtggtg ttgtccaggc catcagtgtc ctgtgtcaga aatatcctcg caaacacgcc 1260  
 gtcttatga acttctgtt caccatgtct cggaagagg gtggtttga gtataagcgc 1320  
 gctatctggg actgcatcat cagcatcatt gaagagaact cagagagcaa ggagacagg 1380  
 ctgtcacatc tgtgcgagtt catcgaggac tgcgagttca cagtgtgtgc caccgtatt 1440  
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 gcgaagtttg gagccagaa tgaagagatg ttaccagta tcttggtgtt gctgaagagg 1620  
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cttccaggaa agggacattg taaatgaata aaacattctc aactcctctt gaatctatcc 3000
cccaagaaac catcttatcc ctgtaataaa tcagcatgta tttattgaaa aaaaaaaaaa 3060
aaaaaaaaaa aaaaaa 3075

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&lt;210&gt; 22

&lt;211&gt; 874

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 22

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Met Leu Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Gly Gly Ser
 1          5          10          15
Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
 20          25          30
Val Phe Asn Glu Thr Pro Ile Asn Pro Arg Lys Cys Ala His Ile Leu
 35          40          45
Thr Lys Ile Leu Tyr Leu Ile Asn Gln Gly Glu His Leu Gly Thr Thr
 50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Lys Leu Phe Gln Ser Asn
 65          70          75          80
Asp Pro Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ser
 85          90          95
Cys Ile Ala Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100          105          110
Met Thr Gly Lys Glu Asp Asn Tyr Arg Gly Pro Ala Val Arg Ala Leu
115          120          125
Cys Gln Ile Thr Asp Ser Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130          135          140
Lys Gln Ala Ile Val Asp Lys Val Pro Ser Val Ser Ser Ser Ala Leu
145          150          155          160
Val Ser Ser Leu His Leu Leu Lys Cys Ser Phe Asp Val Val Lys Arg
165          170          175
Trp Val Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180          185          190
Gln Tyr His Ala Leu Gly Leu Leu Tyr His Val Arg Lys Asn Asp Arg
195          200          205
Leu Ala Val Asn Lys Met Ile Ser Lys Val Thr Arg His Gly Leu Lys
210          215          220
Ser Pro Phe Ala Tyr Cys Met Met Ile Arg Val Ala Ser Lys Gln Leu
225          230          235          240
Glu Glu Glu Asp Gly Ser Arg Asp Ser Pro Leu Phe Asp Phe Ile Glu
245          250          255
Ser Cys Leu Arg Asn Lys His Glu Met Val Val Tyr Glu Ala Ala Ser
260          265          270
Ala Ile Val Asn Leu Pro Gly Cys Ser Ala Lys Glu Leu Ala Pro Ala
275          280          285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Ala Ala Leu Arg
290          295          300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305          310          315          320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Val Thr Asp Ser
325          330          335
Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
340          345          350

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Val Phe Arg Gly Gly His Asp Ile Leu Val Arg Ser Arg Leu Leu Leu  
           835                                  840                                  845  
 Leu Asp Thr Val Thr Met Gln Val Thr Ala Arg Ser Leu Glu Glu Leu  
           850                                  855                                  860  
 Pro Val Asp Ile Ile Leu Ala Ser Val Gly  
           865                                  870

<210> 23  
 <211> 3110  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
       synthetic construct

<400> 23  
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 atgattaaaa aattcgacaa gaaggacgag gagtctggta gtggctccaa tcctttccag 120  
 catctggaga agagtgtgt tttacaggag gctcgtatat tcaatgaaac tccaatcaat 180  
 ccaagaagat gtttgcata tcttacaaag attctttact tactgaacca gggatgaacac 240  
 tttggaacaa cggaagctac agaagccttc tttgcaatga cgcgattgtt tcaatctaata 300  
 gatcaaacat tgaggagaat gtgctacctt accatcaaag aaatggctac catctctgag 360  
 gatgtgataa ttgtcacaag cagtctgact aaagacatga ctggaaaaga agatgtatac 420  
 cgaggcccg ccatcagagc tctctgcagg atcaccgatg gaacaatgtt gcaagccatt 480  
 gaaagataca tgaagcaggc cattgtggat aaagtttcca gtgtatccag ttcagcactg 540  
 gtatcttccc tgcacatgat gaagataagc tatgatgtgg ttaagcgctg gatcaatgaa 600  
 gcccagaag ctgcatcaag tgataatatt atggtccagt accatgcatt gggagtcctg 660  
 tatcacctta gaaagaatga tgcacttgct gtttccaaga tgttgaataa gtttactaaa 720  
 tctgggtctca agtcacagtt tgcttactgc atgctgatcc gaattgccag tcgcttacta 780  
 aaagaaactg aggatggcca tgaaagtcca ctgtttgatt tcattgagag ctgcttgcca 840  
 aataaacatg aaatgggtat ttatgaagct gcttcagcta tcatccatct tcctaactgc 900  
 actgcaagag agttggcacc tgctgtttca gttcttcaac ttttctgtag ttctcctaag 960  
 ccagccttga gatatgcagc tgtgaggacc ttgaacaagg tggcaatgaa gcacccctct 1020  
 gctgttactg cctgcaatct ggacttagaa aacttaatac cagactcaaa cagaagcatt 1080  
 gctaccttag ccattactac actcctcaaa acaggaagtg agagcagtgt ggaccggctc 1140  
 atgaagcaga tatcttcttt tgtgtctgaa atctcagatg agttcaaggt ggtggttgta 1200  
 caggcaatta gtgtctctgt tcagaaatac cctcgaaagc acagtgtcat gatgactttc 1260  
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 gaattcattg aggactgtga acacactgtt ctggctacta agattctaca cttgttgggc 1440  
 aaagagggcc ctagaacgcc tgtccctccc aaatatatcc gttttatatt taatagggtt 1500  
 gtccctggaga atgaggtgtt cagagctgct gctgtgagtg ctttggctaa atttggggct 1560  
 cagaatgaga gtcttctccc aagcatcctt gtactcttac agagggtgat gatggatact 1620  
 gatgacgagg tacgagacag agctaccttc tatctgaatg tgctgcagca gaggcagatg 1680  
 gcactaaatg ccacatatat cttaaatggt ttgacggctc ctgtaccagg gatggaaaaa 1740  
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 gagaagttgg ctcttccag gcaagacatt ttccaagaac aattggctgc cattcctgag 1920  
 tttctgaata taggacctt gttcaagtct tctgagcctg ttcaacttac agaagcagag 1980  
 acagaatatt ttgttcgatg tatcaagcac atgtttacca atcacatcgt gttccagttt 2040  
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 ggaatatgtt acactcttgt tcgtttgcct gatgatgacc ctacagcagt tgcaggctcc 2220  
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 gaggatgggt atgatgtga gtatgtgctg gaagatctcg aagtgtgtgt gtctgacct 2340  
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 gagaaagagg aaacctttgc cctcagttct accaaaacc ttgaagaggc tgtcaacaat 2460  
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 aattcccatt cgctctatct ggcaggtata ttcagaggtg gctatgattt attggtgagg 2580  
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acacctgtag atgttatctt agcttctgtt ggataaatgc ttactggaca agaggaaact 2700
gatgcacact acatgggtcag tgggctttta ggctagtggc atcagtttcc cagaatcaga 2760
cttttgaaga tgaatgactt tggagaagca aattaaacat ttggccctga gccagcagat 2820
caagcaaagt tctatctttg cgcattgggtt gttttttttt tttttctttt tattctactt 2880
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tggaaaattt ttatcccaga ggggtggggg ggagggggga ggggaagcca gagtccactt 3060
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&lt;210&gt; 24

&lt;211&gt; 871

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 24

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Met Ile Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Ser Gly Ser
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Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
20          25          30
Ile Phe Asn Glu Thr Pro Ile Asn Pro Arg Arg Cys Leu His Ile Leu
35          40          45
Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly Glu His Phe Gly Thr Thr
50          55          60
Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Arg Leu Phe Gln Ser Asn
65          70          75          80
Asp Gln Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ala
85          90          95
Thr Ile Ser Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100         105         110
Met Thr Gly Lys Glu Asp Val Tyr Arg Gly Pro Ala Ile Arg Ala Leu
115         120         125
Cys Arg Ile Thr Asp Gly Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130         135         140
Lys Gln Ala Ile Val Asp Lys Val Ser Ser Val Ser Ser Ala Leu
145         150         155         160
Val Ser Ser Leu His Met Met Lys Ile Ser Tyr Asp Val Val Lys Arg
165         170         175
Trp Ile Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180         185         190
Gln Tyr His Ala Leu Gly Val Leu Tyr His Leu Arg Lys Asn Asp Arg
195         200         205
Leu Ala Val Ser Lys Met Leu Asn Lys Phe Thr Lys Ser Gly Leu Lys
210         215         220
Ser Gln Phe Ala Tyr Cys Met Leu Ile Arg Ile Ala Ser Arg Leu Leu
225         230         235         240
Lys Glu Thr Glu Asp Gly His Glu Ser Pro Leu Phe Asp Phe Ile Glu
245         250         255
Ser Cys Leu Arg Asn Lys His Glu Met Val Ile Tyr Glu Ala Ala Ser
260         265         270
Ala Ile Ile His Leu Pro Asn Cys Thr Ala Arg Glu Leu Ala Pro Ala
275         280         285
Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Pro Ala Leu Arg
290         295         300
Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305         310         315         320
Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Ile Thr Asp Ser
325         330         335

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Asn	Arg	Ser	Ile	Ala	Thr	Leu	Ala	Ile	Thr	Thr	Leu	Leu	Lys	Thr	Gly	340	345	350
Ser	Glu	Ser	Ser	Val	Asp	Arg	Leu	Met	Lys	Gln	Ile	Ser	Ser	Phe	Val	355	360	365
Ser	Glu	Ile	Ser	Asp	Glu	Phe	Lys	Val	Val	Val	Val	Gln	Ala	Ile	Ser	370	375	380
Ala	Leu	Cys	Gln	Lys	Tyr	Pro	Arg	Lys	His	Ser	Val	Met	Met	Thr	Phe	385	390	395
Leu	Ser	Asn	Met	Leu	Arg	Asp	Asp	Gly	Gly	Phe	Glu	Tyr	Lys	Arg	Ala	405	410	415
Ile	Val	Asp	Cys	Ile	Ile	Ser	Ile	Val	Glu	Glu	Asn	Pro	Glu	Ser	Lys	420	425	430
Glu	Ala	Gly	Leu	Ala	His	Leu	Cys	Glu	Phe	Ile	Glu	Asp	Cys	Glu	His	435	440	445
Thr	Val	Leu	Ala	Thr	Lys	Ile	Leu	His	Leu	Leu	Gly	Lys	Glu	Gly	Pro	450	455	460
Arg	Thr	Pro	Val	Pro	Ser	Lys	Tyr	Ile	Arg	Phe	Ile	Phe	Asn	Arg	Val	465	470	475
Val	Leu	Glu	Asn	Glu	Ala	Val	Arg	Ala	Ala	Ala	Val	Ser	Ala	Leu	Ala	485	490	495
Lys	Phe	Gly	Ala	Gln	Asn	Glu	Ser	Leu	Leu	Pro	Ser	Ile	Leu	Val	Leu	500	505	510
Leu	Gln	Arg	Cys	Met	Met	Asp	Thr	Asp	Asp	Glu	Val	Arg	Asp	Arg	Ala	515	520	525
Thr	Phe	Tyr	Leu	Asn	Val	Leu	Gln	Gln	Arg	Gln	Met	Ala	Leu	Asn	Ala	530	535	540
Thr	Tyr	Ile	Phe	Asn	Gly	Leu	Thr	Val	Ser	Val	Pro	Gly	Met	Glu	Lys	545	550	555
Ala	Leu	His	Gln	Tyr	Thr	Leu	Glu	Pro	Ser	Glu	Lys	Pro	Phe	Asp	Met	565	570	575
Lys	Ser	Ile	Pro	Leu	Ala	Met	Ala	Pro	Val	Phe	Glu	Gln	Lys	Ala	Glu	580	585	590
Ile	Thr	Leu	Val	Ala	Thr	Lys	Pro	Glu	Lys	Leu	Ala	Pro	Ser	Arg	Gln	595	600	605
Asp	Ile	Phe	Gln	Glu	Gln	Leu	Ala	Ala	Ile	Pro	Glu	Phe	Leu	Asn	Ile	610	615	620
Gly	Pro	Leu	Phe	Lys	Ser	Ser	Glu	Pro	Val	Gln	Leu	Thr	Glu	Ala	Glu	625	630	635
Thr	Glu	Tyr	Phe	Val	Arg	Cys	Ile	Lys	His	Met	Phe	Thr	Asn	His	Ile	645	650	655
Val	Phe	Gln	Phe	Asp	Cys	Thr	Asn	Thr	Leu	Asn	Asp	Gln	Leu	Leu	Glu	660	665	670
Lys	Val	Thr	Val	Gln	Met	Glu	Pro	Ser	Asp	Ser	Tyr	Glu	Val	Leu	Ser	675	680	685
Cys	Ile	Pro	Ala	Pro	Ser	Leu	Pro	Tyr	Asn	Gln	Pro	Gly	Ile	Cys	Tyr	690	695	700
Thr	Leu	Val	Arg	Leu	Pro	Asp	Asp	Asp	Pro	Thr	Ala	Val	Ala	Gly	Ser	705	710	715
Phe	Ser	Cys	Thr	Met	Lys	Phe	Thr	Val	Arg	Asp	Cys	Asp	Pro	Asn	Thr	725	730	735
Gly	Val	Pro	Asp	Glu	Asp	Gly	Tyr	Asp	Asp	Glu	Tyr	Val	Leu	Glu	Asp	740	745	750
Leu	Glu	Val	Thr	Val	Ser	Asp	His	Ile	Gln	Lys	Val	Leu	Lys	Pro	Asn	755	760	765
Phe	Ala	Ala	Ala	Trp	Glu	Glu	Val	Gly	Asp	Thr	Phe	Glu	Lys	Glu	Glu	770	775	780
Thr	Phe	Ala	Leu	Ser	Ser	Thr	Lys	Thr	Leu	Glu	Glu	Ala	Val	Asn	Asn	785	790	795
Ile	Ile	Thr	Phe	Leu	Gly	Met	Gln	Pro	Cys	Glu	Arg	Ser	Asp	Lys	Val	805	810	815

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Pro Glu Asn Lys Asn Ser His Ser Leu Tyr Leu Ala Gly Ile Phe Arg  
 820 825 830  
 Gly Gly Tyr Asp Leu Leu Val Arg Ser Arg Leu Ala Leu Ala Asp Gly  
 835 840 845  
 Val Thr Met Gln Val Thr Val Arg Ser Lys Glu Arg Thr Pro Val Asp  
 850 855 860  
 Val Ile Leu Ala Ser Val Gly  
 865 870

<210> 25  
 <211> 1900  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 25  
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 caagtactat gacgacacct accccagtgt caaggagcaa aaggcctttg agaagaacat 180  
 tttcaacaag acccatcgga ctgacagtga aattgccctc ttggaaggcc tgacagtggg 240  
 atacaaaagc agtatagatc tctatttcta tgtgattggc agctcctatg aaaatgagct 300  
 gatgcttatg gctgttctga actgtctctt cgactcattg agccagatgc tgaggaaaaa 360  
 tgtagaaaag cgagcactgc tggagaacat ggaggggctg ttcttggctg tggatgaaat 420  
 tgtagatgga ggggtgatcc tagagagtga tccccagcag gtggtacacc ggggtggcatt 480  
 aaggggtgaa gatgtcccc ttacggagca gaccgtgtct cagggtgctgc agtcagccaa 540  
 agaacagatc aagtggtcac tccttcgggtg aagacctcac tgttctctggc tcttcctcct 600  
 cttcaaaaaa tttgcatgtc tgctgtgaat tttcatctag ttccccaatc gatgctctca 660  
 ggggtcatctc ggggatcaca gggatcctta aatctccatt ctgtttgtgg ttgccccctc 720  
 aacctcccc acaccttcc tattcttttt cattcttctt gcagttcttg gagtaaagct 780  
 cccagcatat ttagataata gggcagggga agcaccctct ttctttctag actggattat 840  
 gctcacatgc tcccttgccc tgacattttt gtaaattctg tgccctttgc tgtagctaca 900  
 cttcagatta aagtaggaga aagaatgtgc tgagtgtttt cctccctttg cctctacctg 960  
 gccctcatcc caacagccca gcaaggggag agagaaagag aattcttttc tatagaacga 1020  
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 cagtgttttc ttccattcct tcttactgcc ctgtcctctg ccttggaaga ggctttggga 1140  
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 ggtttgtctt ctctgtgtcc tggagcaaag ccagttccta aaactaaaac tccattctag 1380  
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 cagtcgtgc aacctaccct ctctctgcct cagccttaca cccaagcagt aggtctgtgc 1560  
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<210> 26  
 <211> 177  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 26

Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile  
 1 5 10 15  
 Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp  
 20 25 30  
 Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile  
 35 40 45  
 Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly  
 50 55 60  
 Leu Thr Val Val Tyr Lys Ser Ser Ile Asp Leu Tyr Phe Tyr Val Ile  
 65 70 75 80  
 Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ala Val Leu Asn Cys  
 85 90 95  
 Leu Phe Asp Ser Leu Ser Gln Met Leu Arg Lys Asn Val Glu Lys Arg  
 100 105 110  
 Ala Leu Leu Glu Asn Met Glu Gly Leu Phe Leu Ala Val Asp Glu Ile  
 115 120 125  
 Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Val His  
 130 135 140  
 Arg Val Ala Leu Arg Gly Glu Asp Val Pro Leu Thr Glu Gln Thr Val  
 145 150 155 160  
 Ser Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu Leu  
 165 170 175  
 Arg

&lt;210&gt; 27

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 27

Cys Glu Ser Gly Glu Leu Lys Pro Glu Asp Asp Val Thr Val Gly Pro  
 1 5 10 15  
 Ala Gln Lys

&lt;210&gt; 28

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 28

Gly Asn Met Phe Ala Asn Leu Phe Lys Gly Leu Phe Gly Lys Lys Glu  
 1 5 10 15

&lt;210&gt; 29

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 29

Glu Lys Lys Gly Phe Leu Gly Lys Phe Leu Asn Ala Phe Met Asn Gly  
 1 5 10 15

<210> 30

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 30

Cys Thr His Pro Phe Thr His Glu Cys Gly Gly Gly Ser  
 1 5 10

<210> 31

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 31

Cys Gly Glu His Val Arg Pro Ser Cys Gly Gly Gly Ser  
 1 5 10

<210> 32

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 32

Cys Asn Asn Thr Arg Ser Pro Tyr Cys Gly Gly Gly Ser  
 1 5 10

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 33

Cys Glu Gln Thr Leu Tyr Arg Val Cys Gly Gly Gly Ser  
 1 5 10

<210> 34  
 <211> 3916  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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<400> 34
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gagtgcggggc gcgccccacc accgccctca ccatgggtgct gttggcagca gcggtctgca      180
caaaagcagg aaaggtctatt gtttctcgac agtttgtgga aatgacccga actcggattg      240
agggtcttatt agcagctttt ccaaagctca tgaacactgg aaaacaacat acgtttgttg      300
aaacagagag tgtaagatat gtctaccagc ctatggagaa actgtatatg gtactgatca      360
ctacaaaaaa cagcaacatt ttagaagatt tggagaccct aaggctcttc tcaagagtga      420
tccctgaata ttgccgagcc ttagaagaga atgaaatata tgagcactgt tttgatttga      480
tttttgcctt tgatgaaatt gtcgcactgg gataccggga gaatgttaac ttggcacaga      540
tcagaacctt cacagaaatg gattctcatg aggagaaggt gttcagagcc gtcagagaga      600
ctcaagaacg tgaagctaag gctgagatgc gtcgtaaagc aaaggaatta caacaggccc      660
gaagagatgc agagagacag ggcaaaaaag caccaggatt tggcggattt ggcagctctg      720
cagtatctgg aggcagcaca gctgccatga tcacagagac catcattgaa actgataaac      780
caaaagtggc acctgcacca gccaggcctt caggccccag caaggcttta aaacttggag      840
ccaaaggaaa ggaagtagat aactttgtgg acaaattaaa atctgaaggt gaaaccatca      900
tgtcctctag tatgggcaag cgtacttctg aagcaaccaa aatgcatgct ccaccatta      960
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&lt;210&gt; 35

&lt;211&gt; 511

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 35

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Val Ser Arg Gln Phe Val Glu Met Thr Arg Thr Arg Ile Glu Gly Leu
          20          25          30
Leu Ala Ala Phe Pro Lys Leu Met Asn Thr Gly Lys Gln His Thr Phe
          35          40          45
Val Glu Thr Glu Ser Val Arg Tyr Val Tyr Gln Pro Met Glu Lys Leu
          50          55          60
Tyr Met Val Leu Ile Thr Thr Lys Asn Ser Asn Ile Leu Glu Asp Leu
          65          70          75          80
Glu Thr Leu Arg Leu Phe Ser Arg Val Ile Pro Glu Tyr Cys Arg Ala
          85          90          95
Leu Glu Glu Asn Glu Ile Ser Glu His Cys Phe Asp Leu Ile Phe Ala
          100          105          110
Phe Asp Glu Ile Val Ala Leu Gly Tyr Arg Glu Asn Val Asn Leu Ala
          115          120          125
Gln Ile Arg Thr Phe Thr Glu Met Asp Ser His Glu Glu Lys Val Phe
          130          135          140
Arg Ala Val Arg Glu Thr Gln Glu Arg Glu Ala Lys Ala Glu Met Arg
          145          150          155          160
Arg Lys Ala Lys Glu Leu Gln Gln Ala Arg Arg Asp Ala Glu Arg Gln
          165          170          175
Gly Lys Lys Ala Pro Gly Phe Gly Gly Phe Gly Ser Ser Ala Val Ser
          180          185          190
Gly Gly Ser Thr Ala Ala Met Ile Thr Glu Thr Ile Ile Glu Thr Asp
          195          200          205
Lys Pro Lys Val Ala Pro Ala Pro Ala Arg Pro Ser Gly Pro Ser Lys
          210          215          220
Ala Leu Lys Leu Gly Ala Lys Gly Lys Glu Val Asp Asn Phe Val Asp
          225          230          235          240
Lys Leu Lys Ser Glu Gly Glu Thr Ile Met Ser Ser Ser Met Gly Lys
          245          250          255
Arg Thr Ser Glu Ala Thr Lys Met His Ala Pro Pro Ile Asn Met Glu
          260          265          270

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Ser	Val	His	Met	Lys	Ile	Glu	Glu	Lys	Ile	Thr	Leu	Thr	Cys	Gly	Arg		
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Asp	Gly	Gly	Leu	Gln	Asn	Met	Glu	Leu	His	Gly	Met	Ile	Met	Leu	Arg		
	290					295					300						
Ile	Ser	Asp	Asp	Lys	Tyr	Gly	Arg	Ile	Arg	Leu	His	Val	Glu	Asn	Glu		
305					310				315						320		
Asp	Lys	Lys	Gly	Val	Gln	Leu	Gln	Thr	His	Pro	Asn	Val	Asp	Lys	Lys		
			325						330					335			
Leu	Phe	Thr	Ala	Glu	Ser	Leu	Ile	Gly	Leu	Lys	Asn	Pro	Glu	Lys	Ser		
			340					345					350				
Phe	Pro	Val	Asn	Ser	Asp	Val	Gly	Val	Leu	Lys	Trp	Arg	Leu	Gln	Thr		
		355					360						365				
Thr	Glu	Glu	Ser	Phe	Ile	Pro	Leu	Thr	Ile	Asn	Cys	Trp	Pro	Ser	Glu		
	370					375					380						
Ser	Gly	Asn	Gly	Cys	Asp	Val	Asn	Ile	Glu	Tyr	Glu	Leu	Gln	Glu	Asp		
385					390					395					400		
Asn	Leu	Glu	Leu	Asn	Asp	Val	Val	Ile	Thr	Ile	Pro	Leu	Pro	Ser	Gly		
			405						410					415			
Val	Gly	Ala	Pro	Val	Ile	Gly	Glu	Ile	Asp	Gly	Glu	Tyr	Arg	His	Asp		
		420						425					430				
Ser	Arg	Arg	Asn	Thr	Leu	Glu	Trp	Cys	Leu	Pro	Val	Ile	Asp	Ala	Lys		
	435						440					445					
Asn	Lys	Ser	Gly	Ser	Leu	Glu	Phe	Ser	Ile	Ala	Gly	Gln	Pro	Asn	Asp		
	450					455					460						
Phe	Phe	Pro	Val	Gln	Val	Ser	Phe	Val	Ser	Lys	Lys	Asn	Tyr	Cys	Asn		
465					470				475						480		
Ile	Gln	Val	Thr	Lys	Val	Thr	Gln	Val	Asp	Gly	Asn	Ser	Pro	Val	Arg		
			485						490					495			
Phe	Ser	Thr	Glu	Thr	Thr	Phe	Leu	Val	Asp	Lys	Tyr	Glu	Ile	Leu			
		500						505					510				